```
(5')    1   SDLEQERRAKEKLQEQQ
       18   SDLEQDRLAKEKLQEQQ
       35   SDLEQERLAKEKLQEQQ
       52   SDLEQERRAKEKLQEQQ
       69   SDLEQERRAKEKLQEQQ
       86   SDLEQDRLAKEKLQEQQ
      103   SDLEQERRAKEKLQEQQ
      120   SDLEQERKAKEKLQEQQ
      137   SDLEQERLAKEKLQEQQ
      154   SDLEQERRAKEKLQEQQ
      171   SDLEQERRAKEKLQEQQ
      188   SDLEQERRAKEKLQEQQ
      205   RDLEQ

      210   RKADTKKNLERKKEHGDILAEDLYGRLEIP
      240   AIELPSENERGYYIPHQSSLPQDNRGNSRD
      270   SKEISIIEKTNRESITTNVEGRRDIHKGHL
      300   EEKKDGSIKPEQKEDKS      316 (3')
```

FIGURE 1

```
(5')   1  AAAGCGATCTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
      52  AAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
     103  AAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
     154  AAAGCGATCTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     205  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     256  AAAGCGATTTAGAACAAGAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
     307  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     358  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     409  AAAGCGATTTAGAACAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAC
     460  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     511  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC
     562  AAAGCGATTTAGAACAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC
     613  AAAGAGATTTAGAACAA
     630  AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
     681  ATATTAGCAGAGGATTTATATGTCGTTTAGAAATACCAGCTATAGAACTT
     732  CCATCAGAAAATGAACGTGGATATTATTATATACCACATCAATCTTCTTACCT
     783  CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
     834  AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
     885  CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA
     936  AAAGAAGATAAATCT   950   (3')
```

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQQEQQ

HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI

ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE

ESVAPSVEESVAEMLKER

FIGURE 3

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT
GTT AAT GGA GAA GTA AAA GAA AAT ATT TTG GAG GAA AGT CAA GTT AAT
GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA
CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG
AAG AAA GTG TAG AAG AAG ATG AAG AAG ATG TAG AAG GTA TAG AAA ATG
ACG ACG GAA GTG TAG CCT CAA GTG TTG AAG GTA TAG CTT CAA GTG
TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG ATG TAG CTC CAA CTG
TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG TTG TAG CTC CAA GTG
TTG TAG AAA AGT TAG GTC CAA GTG TTG AAG GTG TAG CTC CAA GTG
TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

LSA-TER

729S-NRI
729S-NRII
729S-Rep

NSRDSKEISIIEKTNRESITTNVEGRRDIHK

DELFNELLNSVDVNGEVKENILEESQ
LEESQVNDDIFSNSLVKSVQQEQQHNV
VEKCAPSVEESVAPSVEESVAEMLKER

FIGURE 5

NUCLEOTIDE SEQUENCE OF THE LSA GENE
5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
84 ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA
186 GGAAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAACT
237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT
288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAAGTCTTTTAAGAAATCT
339 TGGTGTTTCAGAGAATATATTCCTTAAAGAAAATAAATTAAATAAGGAAGGG
390 AAATTAATTGAACACATAATAAATGATGATGACGATAAAAAAAAATATATTA
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGT
543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
594 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT
900 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

FIGURE 6

LSA.5'/ATG - -> 1-phase Translation

DNA sequence   956 b.p.   ATGAAACATATT ... AAGGGATTTAGA   linear

```
1 / 1                                    31 / 11
ATG AAA CAT ATT TTG TAC ATA TCA TTT TAC  TTT ATC CTT GTT AAT TTA TTG ATA TTT CAT
met lys his ile leu tyr ile ser phe tyr  phe ile leu val asn leu leu ile phe his

61 / 21                                   91 / 31
ATA AAT GGA AAG ATA ATA GAA ATC ATA AAA  TCT AAC TTG AGA ...
ile asn gly lys ile ile glu ile ile lys  ser asn leu arg ...

121 / 41                                  151 / 51
AGT GGT TCT TCA AAT TCT AGG AAT CGA ATA  ... GAG AAG AAA CAC GTT
ser gly ser ser asn ser arg asn arg ile  ... glu lys lys his val

181 / 61                                  211 / 71
TTA TCT CAT AAT TCA TAT GAG AAA ACT ...  AAA AAT AAT AAA ... TTT GAT AAG
leu ser his asn ser tyr glu lys thr ...  lys asn asn lys ... phe asp lys

241 / 81                                  271 / 91
GAT AAA GAG TTA ACG ATG TCT AAT GTA ...  AAT GTG TCA CAA ACA AAT TTC AAA AGT CTT
asp lys glu leu thr met ser asn val ...  asn val ser gln thr asn phe lys ser leu

301 / 101                                 331 / 111
TTA AGA AAT CTT GGT GTT TCA GAG AAT ...  ATA TTC CTT AAA GAA AAT TTA AAT AAG GAA
leu arg asn leu gly val ser glu asn ...  ile phe leu lys glu asn leu asn lys glu
```

FIGURE 7A

```
361 /
121 /  GGG AAA TTA ATT GAA CAC ATA ATA AAT GAT
       gly lys leu ile glu his ile ile asn asp
391 / 131
       GAT GAC GAT AAA AAA AAA TAT ATT AAA GGG
       asp asp asp lys lys lys tyr ile lys gly
421 / 141
       CAA GAC GAA AAC AGA CAA GAA GCA AAA GCT
       gln asp glu asn arg gln glu ala lys ala
451 / 151
       GAT ... ...
481 / 161
       GAA GAT GCT GAA TCA GAA GAG CAA CAA CAA
       glu asp ... glu ... ... ... gln gln gln
511 / 171
       ... AGC CAA AGC ...
       ... ser gln ser ...
541 / 181
       CAA AGC GAT TCA GAA GAG ...
       gln ser asp ser glu glu ...
571 / 191
       GAT CAA GAG CAA GAG CTT AGA GCT AAA TTA GAA
       asp gln glu gln glu leu arg ala lys leu glu
601 / 201
       GAA TTA GCT CTT AGA TTA GAA AAA GCT AGC
       glu leu ala leu arg leu glu lys ala ser
631 / 211
       CAA AAA GAA GAA TTG GAT TTA GAA CAA GAG
       gln lys glu glu leu asp leu glu gln glu
661 / 221
       GAG GAA CGT GCT AAA GAG AGA CAA GAG AGA
       glu glu arg ala lys glu arg gln glu arg
691 / 231
       CAA GAG AGA GAA TTG CAA AAG TTA GAA GAG
       gln glu arg glu leu gln lys leu glu glu
721 / 241
       CTT GCT AAA GCT CGT GCT AAA GAA GAA AAG
       leu ala lys ala arg ala lys glu glu lys
751 / 251
       GAA AAG TTG CAA GAA CAA CAA GAT TTA GAA AAG TTG
       glu lys leu gln glu gln gln asp leu glu lys leu
```

FIGURE 7B

```
781 / 261
CAA GAA CAA AGC GAT TTA GAA AAG TTA CAA GAG CAG
gln glu gln ser asp leu glu lys leu gln glu gln

811 / 271
GAA CAA GAG CTT GCT AAA GAA AAG TTA CAA GAG CAG
glu gln glu leu ala lys glu lys leu gln glu gln

841 / 281
CAA AGC GAT TTA GAA CTT GCT AAA GAA TTG CAA GAA CAA
gln ser asp leu glu leu ala lys glu leu gln glu gln

871 / 291
AGA CTT GCT AAA GAA AAG TTA CAA CAA AGC GAT
arg leu ala lys glu lys leu gln gln ser asp

901 / 301
TTA GAA CAA CAA AGG TTG CAA GAA CAA AGC GAT TTA
leu glu gln gln arg leu gln glu gln ser asp leu

931 / 311
AAA GAA CGT GCT AAA GAA CAA CAA AGC GAT TTA
lys glu arg ala lys glu gln gln ser asp leu
```

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE
3' END

(CODING 3' END, REPETITIVE)

```
1   CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
37  GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
88  GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
190 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
241 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
343 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
445 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
598 GCTAAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA
```

(CODING 3' END, UNIQUE)

```
640  AGGAAGGCTGATACGAAAAAAAATTTAGAAAGAAAAAAGGAACATGGÁGAT
691  ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
742  CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
793  CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
844  AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
895  CATAAAGGACATCTTGAAGAAAGAAAGATGGTTCAATAAAACCAGAACAA
946  AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT
997  ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
1252 AAAAAATAAAAAAAGGAAAGAAATATGAAAAAACAAAGGATAATAATTTTA
1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA
1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
1456 ATATAACTAAATATTTTATGAAACTA**TAA** (stop)
```

(NON-CODING 3' END)

```
1485 AAGGTTATATATTT 1498
```

FIGURE 8

LSA.3'.ALL -> 1-phase Translation

DNA sequence 1496 b.p.   CAAGAACAACAA ... GGTTATATATT   linear

```
1 / 1
CAA GAA CAA CAA AGC GAT CTA GAA CAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA
gln glu gln gln ser asp leu glu gln gln glu arg arg ala lys glu lys leu gln glu gln
61 / 21                  91 / 31
CAA AGC GAT TTA GAA CAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT
gln ser asp leu glu gln gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp
121 / 41                 151 / 51
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA CAA CAA CTA GAA GAA CAA
leu glu gln glu arg leu ala lys glu lys leu gln glu gln gln gln gln leu glu glu gln
181 / 61                 211 / 71
GAG AGA CGT AAA GAA GAA GGG AAA GAA AAG TTG CAA GAA CAA CAA CAA AGC GAT TTA GAA CAA CGT
glu arg arg lys glu glu glu lys glu lys leu gln glu gln gln gln ser asp leu glu glu arg
241 / 81                 271 / 91
GCT AAA GAA GAA TTG CAA CAA CAA GAA CAA CAA GAT AGA CAA GAT TTA GCT AAA GAA
ala lys glu glu leu gln gln gln glu gln gln asp arg gln asp leu ala lys glu
301 / 101                331 / 111
AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA CAA GAA AAG TTG CAA
lys leu gln glu gln gln ser asp leu glu gln gln glu lys leu gln
```

FIGURE 9A

```
361 /              391 / 131
GAA CAA AGC GAT TTA    GAA CAA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA
glu gln ser asp leu    glu gln arg ala lys glu lys leu gln glu gln gln

421 / 141          451 / 151
AGC GAT TTA GAG CAA CTT    GCT CAA AAG GAA TTG CAA CAA CAA GAT AGC GAT TTA
ser asp leu glu gln leu    ala gln lys glu leu gln gln gln asp ser asp leu

481 / 161          511 / 171
GAA CAA CGT GCT    AAA GAA AAG TTG CAA GAA CAA GAG
glu gln arg ala    lys glu lys leu gln glu gln glu

541 / 181          571 / 191
GAA CAA CGT GCT AGA CAA AAG    TTG GAA GAG CAA GAA GAA CAA GAG AGA CGT GCT
glu gln arg ala arg gln lys    leu glu glu gln glu glu gln glu arg arg ala

601 / 201          631 / 211
AGA CGT GCT    CAA GAA GAT TTA GAA CAA CAA GAG CGT GCT
arg arg ala    gln glu asp leu glu gln gln glu arg arg ala

661 / 221          691 / 231
AAA GAA AAG TTG    GAA CAA CAA AGG ACG AAA AAA
lys glu lys leu    glu gln gln arg thr lys lys

721 / 241          751 / 251
TTA GAA GAT ATA    GGA GAG TTA GCA GAT TTA TAT TAT GGT CGT
leu glu asp ile    gly glu leu ala asp leu tyr tyr gly arg

781 / 261
GAA ATA CCA GCT ATA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT
glu ile pro ala ile glu asn glu arg gly tyr tyr ile pro his
TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG ATA ATA    811 / 271
ser leu pro gln asp asn arg gly asn ser arg asp ser lys ile ile
```

FIGURE 9B

```
 841                                            871
GAA AAA ACA AAT GTT GAA GGA CGA GAT ATA   CAT AAA
glu lys thr asn val glu gly arg asp ile   his lys
 281                                            291

 901                                            931
GGA CAT CTT GAA GAA AAG GAT AAA GAA CAA   GAT AAA TCT
gly his leu glu glu lys asp lys glu gln   asp lys ser
 301                                            311

 961                                            991
GCT GAC ATA CAA AAT CAT AAT CAT ACA GAG   TTA GTA GTT  GAT TTT CAA
ala asp ile gln asn his asn his thr glu   leu val val  asp phe gln
 321                                            331

1021                                           1051
ATA AGT AAG TAT GAG GAT GCT GAA ATA AGT   TTA ATA GAT  GAT GAA GAA
ile ser lys tyr glu asp ala glu ile ser   leu ile asp  asp glu glu
 341                                            351

1081                                           1111
GAT GAA GAC TTA GAC GAA TTT AAG CCT ATT   GTG CAA TAT  TTC CAA GAT
asp glu asp leu asp glu phe lys pro ile   val gln tyr  phe gln asp
 361                                            371

1141                                           1171
GAA GAT GAA GAC TTA GAA GAT GAA AAA ATA   GGA GAG ATA  AAT AAT TTA
glu asp glu asp leu glu asp glu lys ile   gly glu ile  asn asn leu
 381                                            391

1201                                           1231
GAA GAA AAC ATA GAA GGA ATA TCA GAA AAA   TCA GAA TTA  ATA ATA AAA
glu glu asn ile glu gly ile ser glu lys   ser glu leu  ile ile lys
 401                                            411

GAT GAT TTA GAT GAA GAA
asp asp leu asp glu glu
```

FIGURE 9C

```
1261 / 421
AAA GGA AAG AAA TAT GAA AAG ACA AAA GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
lys gly lys lys tyr glu lys thr lys asp asn asn phe lys pro asn asp lys ser leu

1321 / 441
TAT GAT GAG CAT ATT AAA AAA TAT AAA AAT GAT AAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys lys tyr lys asn asp lys val asn lys glu lys glu lys

1381 / 461
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp

1441 / 481
GAG TTA TCT GAA ATA GAT ATA TTT ATG AAA CTA AAA TAA GTT ATA TAT
glu leu ser glu ile asp ile phe met lys leu lys OCH val ile tyr
```

FIGURE 9D

LSN.3'STOP -> 1-phase Translation

DNA sequence   1482 b.p.   CAAGAACAACAA ... ATGAAACTATAA   linear

```
1 / 1                                                       31 / 11
CAA GAA CAA AGC GAT CAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA GAA
gln glu gln ser asp gln gln glu arg arg ala lys glu lys leu gln glu gln
61 / 21                                                     91 / 31
CAA AGC GAT TTA GAA CAA CTT AGA GAT AGA CGT GCT AAA GAA AAG TTA CAA AGC GAT
gln ser asp leu glu gln leu arg asp arg arg ala lys glu lys leu gln ser asp
121 / 41                                                    151 / 51
TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA CAA CAA CAA CTA GAA CAA
leu glu gln glu arg leu ala lys glu lys leu gln gln gln gln leu glu gln
181 / 61                                                    211 / 71
GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA CAA GAT TTA GAA CAA GAG AGA CGT
glu arg arg ala lys glu lys leu gln glu gln gln gln asp leu glu gln glu arg arg
241 / 81                                                    271 / 91
GCT AAA GAA AAG TTG CAA GAA CAA CAA CAA AGC GAT AGA CTT GCT AAA GAA
ala lys glu lys leu gln glu gln gln gln ser asp arg leu ala lys glu
301 / 101                                                   331 / 111
AAG TTA CAA GAG CAG CAA CAA GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA TTG CAA
lys leu gln glu gln gln gln asp leu glu gln glu arg arg ala lys glu leu gln
```

FIGURE 10A

```
(side label, rotated)  top pro hev 860

361  GAA CAA AGC GAT TTA GAA CAA AGA CGT GCT
121  glu gln ser asp leu glu gln arg arg ala

391  GAG CAA GAG GCT GCT AAA GAA AAG TTG CAA
131  glu gln glu ala ala lys glu lys leu gln

421  GAA CAA CAA CAA CAA CAA CAA GAT TTA CAA
141  glu gln gln gln gln gln gln asp leu gln

451  AGA CTT GCT AGA GAG CAA CGT GCT AAA GAA
151  arg leu ala arg glu gln arg ala lys glu

481  AGC GAT TTA GAA GAA GAG AGC CAA CAA CAA
161  ser asp leu glu glu glu ser gln gln gln

511  CTT GCT CGT GAT TTA CAA CAA GAA CAA AGC
171  leu ala arg asp leu gln gln glu gln ser

541  GAG CAA CAA GAA TTA GAA GAA GAG GAG CAA
181  glu gln gln glu leu glu glu glu glu gln

571  GCT AAA GAA CAA GAA CAA GAG CAA GAG GCT
191  ala lys glu gln glu gln glu gln glu ala

601  AGA CGT GAA CAA CAA GAA GAG GAT GCT GCT
201  arg arg glu gln gln glu glu asp ala ala

631  AAA GAA TTG CAA GAG GAG CAA AGG GAT ACG
211  lys glu leu gln glu glu gln arg asp thr

661  AAA GAG TTG CAA GAA GAG TTA GCA GAT TTA
221  lys glu leu gln glu glu leu ala asp leu

691  AAA AGA AAG GAA ATA TTA CAT GGA GAT TTA
231  lys arg lys glu ile leu his gly asp leu

721  GAA TTA GAA AAT GAA CGT GGA TAT TAT ATA
241  glu leu glu asn glu arg gly tyr tyr ile

751  CCA CTT CCA TCA GAA AGT GAA GAT CCA CAT
251  pro leu pro ser glu ser glu asp pro his

781  GAA ATA GCT GAA GGG AAT AGA GAT TCC AAG
261  glu ile ala glu gly asn arg asp ser lys

811  TCT CCT TTA CAG GAC AAC AGA GAA ATA ATA
271  ser pro leu gln asp asn arg glu ile ile
```

FIGURE 10B

```
841 /                                                          281 /
GAA AAA ACA AAT AGA GAA GGA CGA AGG GAT ATA CAT AAA
glu lys thr asn arg glu gly arg arg asp ile his lys

871 /                                                          291 /
TCT ATT ACA ACA AAT GTT GAA GGA CAA GAA CCA TCA GAT
ser ile thr thr asn val glu gly gln glu pro ser asp

901 /                                                          301 /
GGA CAT CTT GGT TCA ATA AAA CCA GAA CAA AAA GAA GAT
gly his leu gly ser ile lys pro glu gln lys glu asp

931 /                                                          311 /
AAA GAT CAT GAA CTT GGT TCA ATA AAA CCA GAA CAA AAA
lys asp his glu leu gly ser ile lys pro glu gln lys

961 /                                                          321 /
GCT GAC ATA CAA AAT CAT GTA ACA GAG TTA ATT TCT GTT
ala asp ile gln asn his val thr glu leu ile ser val

991 /                                                          331 /
GAG GAT CTT GAT GAT GTT AAT AAT GTT CCT GAT ATT TCT
glu asp leu asp asp val asn asn val pro asp ile ser

1021 /                                                         341 /
ATA GAT GAC ATA CAA AAT CAT GTA ACA GAG TTA ATA ATA
ile asp asp ile gln asn his val thr glu leu ile ile

1051 /                                                         351 /
GAA ATA GAG ATA TTA GAT ATA GAT TCA GAT GAT TTC CAA
glu ile glu ile leu asp ile asp ser asp asp phe gln

1081 /                                                         361 /
ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT ATA GAG GAA
ile ser lys tyr glu asp glu ile ser ala ile glu glu

1111 /                                                         371 /
GAC GAA TTT AAG CCT ATT GTG CAA AAT TTC AAA GAT GAT
asp glu phe lys pro ile val gln asn phe lys asp asp

1141 /                                                         381 /
TAT AAA GGA GAG CTA GAA GAT TTG ATA GAG AAA AAT TTA
tyr lys gly glu leu glu asp leu ile glu lys asn leu

1171 /                                                         391 /
AAA TAT AAA GAC GAT AAA TCA GAA GGA TAT TCT GAA GAA
lys tyr lys asp asp lys ser glu gly tyr ser glu glu

1201 /                                                         401 /
GAA TTA GAT GAA GAA CTA TCA TCA GAA GAA TTA GAA GAA
glu leu asp glu glu leu ser ser glu glu leu glu glu

1231 /                                                         411 /
GAT ATA GAA AAA TCA AAA TTT ATA AAA CCA ATA AAA ATA
asp ile glu lys ser lys phe ile lys pro ile lys ile

1261 /                                                         421 /
TTA GAT GAA GGA TTA GAT GAG TCT GAA GAA GAT GAT ATA
leu asp glu gly leu asp glu ser glu glu asp asp ile

1291 /                                                         431 /
AAA ACA GAA TAT AAA ACA GAA AAT AAT TTT CCA AAA GAT
lys thr glu tyr lys thr glu asn asn phe pro lys asp
```

FIGURE 10C

```
1321 /  441
TAT GAT GAG CAT ATT AAA AAA TAT AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
tyr asp glu his ile lys  lys tyr asn asp lys gln val asn lys glu lys glu lys
1381 /  461                   1411 /  471
TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GGA GAC AAT GAA ATT TTA CAG ATC GTG GAT
phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
1441 /  481                   1471 /  491
GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr
```

FIGURE 10D